

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/539, 891
Source: PCT.
Date Processed by STIC: 06-29-2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,891

TIME: 14:01:51

Input Set : A:\Sequence Listing for 13478-00001-US.txt

Output Set: N:\CRF4\06292005\J539891.raw

3 <110> APPLICANT: Napier, Johnathan A.
 4 Sayanova, Olga
 5 Lazarus, Colin M.
 6 Qi, Baoxiu
 7 Heinz, Ernst
 8 Zank, Thorsten
 9 Zahringer, Ulrich
 11 <120> TITLE OF INVENTION: Novel method for the production of polyunsaturated fatty acids
 13 <130> FILE REFERENCE: 13478-00001-US
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/539,891
 C--> 15 <141> CURRENT FILING DATE: 2005-06-17
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014054
 16 <151> PRIOR FILING DATE: 2003-12-11
 18 <150> PRIOR APPLICATION NUMBER: GB 0229578.0
 19 <151> PRIOR FILING DATE: 2002-12-19
 21 <150> PRIOR APPLICATION NUMBER: GB 0316989.3
 22 <151> PRIOR FILING DATE: 2003-07-21
 24 <160> NUMBER OF SEQ ID NOS: 10
 26 <170> SOFTWARE: PatentIn version 3.3
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1266
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Euglena gracilis
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)..(1266)
 36 <223> OTHER INFORMATION: delta-8-desaturase
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 41 1 5 10 15
 43 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96
 44 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 45 20 25 30
 47 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144
 48 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 49 35 40 45
 51 cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat 192
 52 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 53 50 55 60
 55 ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag 240
 56 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 57 65 70 75 80

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59 gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat      288
60 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
61                               85                               90                               95
63 gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt      336
64 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
65                               100                              105                              110
67 gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att      384
68 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
69                               115                              120                              125
71 ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct      432
72 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
73                               130                              135                              140
75 cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac      480
76 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
77 145                               150                              155                              160
79 ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca      528
80 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
81                               165                              170                              175
83 tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa      576
84 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
85                               180                              185                              190
87 ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag      624
88 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
89                               195                              200                              205
91 gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc      672
92 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
93                               210                              215                              220
95 cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg      720
96 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
97 225                               230                              235                              240
99 tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac      768
100 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
101                               245                              250                              255
103 caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg      816
104 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
105                               260                              265                              270
107 cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc      864
108 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
109                               275                              280                              285
111 ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc      912
112 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
113                               290                              295                              300
115 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
116 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
117 305                               310                              315                              320
119 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
120 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
121                               325                              330                              335
123 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga      1056

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124 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
125          340          345          350
127 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc 1104
128 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
129          355          360          365
131 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag 1152
132 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
133          370          375          380
135 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc 1200
136 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
137 385          390          395          400
139 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc 1248
140 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
141          405          410          415
143 gcg ggg aag gct cta taa 1266
144 Ala Gly Lys Ala Leu
145          420
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 421
150 <212> TYPE: PRT
151 <213> ORGANISM: Euglena gracilis
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157 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
158          20          25          30
160 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
161          35          40          45
163 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
164          50          55          60
166 Pro Ser Ser Glu Leu Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
167 65          70          75          80
169 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
170          85          90          95
172 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
173          100          105          110
175 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
176          115          120          125
178 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
179          130          135          140
181 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
182 145          150          155          160
184 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
185          165          170          175
187 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
188          180          185          190
190 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
191          195          200          205
193 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe

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194      210      215      220
196 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
197 225      230      235      240
199 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
200      245      250      255
202 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
203      260      265      270
205 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
206      275      280      285
208 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
209      290      295      300
211 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
212 305      310      315      320
214 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
215      325      330      335
217 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
218      340      345      350
220 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
221      355      360      365
223 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
224      370      375      380
226 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
227 385      390      395      400
229 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
230      405      410      415
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233      420
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238 <212> TYPE: DNA
239 <213> ORGANISM: Isochrysis galbana
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242 <221> NAME/KEY: CDS
243 <222> LOCATION: (1)..(777)
244 <223> OTHER INFORMATION: delta-9-elongase
246 <400> SEQUENCE: 3
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249 1 5 10 15
251 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
252 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
253 20 25 30
255 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
256 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
257 35 40 45
259 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
260 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
261 50 55 60
263 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240

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264 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
265 65 70 75 80
267 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
268 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
269 85 90 95
271 tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
272 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
273 100 105 110
275 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384
276 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
277 115 120 125
279 agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432
280 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
281 130 135 140
283 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
284 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
285 145 150 155 160
287 ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
288 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
289 165 170 175
291 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576
292 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
293 180 185 190
295 cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624
296 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
297 195 200 205
299 aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct 672
300 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
301 210 215 220
303 ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt 720
304 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
305 225 230 235 240
307 ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag 768
308 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
309 245 250 255
311 cag ctc tag 777
312 Gln Leu
315 <210> SEQ ID NO: 4
316 <211> LENGTH: 258
317 <212> TYPE: PRT
318 <213> ORGANISM: Isochrysis galbana
320 <400> SEQUENCE: 4
321 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
322 1 5 10 15
324 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
325 20 25 30
327 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
328 35 40 45
330 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/539,891

DATE: 06/29/2005

TIME: 14:01:52

Input Set : A:\Sequence Listing for 13478-00001-US.txt
Output Set: N:\CRF4\06292005\J539891.raw**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 106,121

Seq#:10; Xaa Pos. 106,121

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44
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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:336
M:341 Repeated in SeqNo=9
L:995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:96
M:341 Repeated in SeqNo=10